



AKIMA-DTSV

1 MAR 2005

UNITED STATES PATENT AND TRADEMARK OFFICE

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APPLICATION NUMBER	FILING OR 371 (c) DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NUMBER
10/680,963	10/07/2003	Piotr Bobrowicz	GFI/108

1473
FISH & NEAVE IP GROUP
ROPES & GRAY LLP
1251 AVENUE OF THE AMERICAS FL C3
NEW YORK, NY 10020-1105

CONFIRMATION NO. 6071
FORMALITIES LETTER



OC000000015078740

Date Mailed: 02/01/2005

NOTICE OF INCOMPLETE REPLY (NONPROVISIONAL)***Filing Date Granted***

The U.S. Patent and Trademark Office has received your reply on 12/15/2004 to the Notice to File Missing Parts (Notice) mailed 06/25/2004 and it has been entered into the nonprovisional application. The reply, however, does not include the following items required in the Notice.

The period of reply remains as set forth in the Notice. You may, however, obtain EXTENSIONS OF TIME under the provisions of 37 CFR 1.136 (a) accompanied by the appropriate fee (37 CFR 1.17(a)).

A complete reply must be timely filed to prevent ABANDONMENT of the above-identified application. Replies should be mailed to: Mail Stop Missing Parts, Commissioner for Patents, P.O. Box 1450, Alexandria VA 22313-1450.

The application is informal since it does not comply with the regulations for the reason(s) indicated below.

The required item(s) identified below must be timely submitted to avoid abandonment:

- Replacement drawings in compliance with 37 CFR 1.84 and 37 CFR 1.121 are required. The drawings submitted are not acceptable because:
 - The drawings submitted to the Office are not electronically reproducible. Drawing sheets must be submitted on paper, which is flexible, strong, white, smooth, non-shiny, and durable (see 37 CFR 1.84(e)). See Figure(s) 14, 25-32.
- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

To Download Patentin Software, visit <http://www.uspto.gov/web/patents/software.htm>
 For questions regarding compliance to these requirements, please contact:

- For Rules Interpretation, call (571) 272-0951
- For Patentin Software Program Help, call Patent EBC at 1-866-217-9197 or directly at 703-305-3028 / 703-308-6845 between the hours of 6 a.m. and 12 midnight, Monday through Friday, EST.
- Send e-mail correspondence for Patentin Software Program Help @ ebc@uspto.gov

Replies should be mailed to: Mail Stop Missing Parts
Commissioner for Patents
P.O. Box 1450
Alexandria VA 22313-1450

*A copy of this notice **MUST** be returned with the reply.*



Customer Service Center
Initial Patent Examination Division (703) 308-1202
PART 1 - ATTORNEY/APPLICANT COPY



UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
 United States Patent and Trademark Office
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 P.O. Box 1450
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10/680,963	10/07/2003	Piotr Bobrowicz	GFI/108

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 - The drawings submitted to the Office are not electronically reproducible. Drawing sheets must be submitted on paper, which is flexible, strong, white, smooth, non-shiny, and durable (see 37 CFR 1.84(e)). See Figure(s) 14, 25-32.
- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

To Download Patentin Software, visit <http://www.uspto.gov/web/patents/software.htm>
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- **For Rules Interpretation, call (571) 272-0951**
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- **Send e-mail correspondence for Patentin Software Program Help @ ebc@uspto.gov**

Replies should be mailed to: Mail Stop Missing Parts
Commissioner for Patents
P.O. Box 1450
Alexandria VA 22313-1450

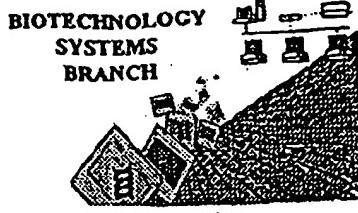
*A copy of this notice **MUST** be returned with the reply.*



Customer Service Center

Initial Patent Examination Division (703) 308-1202

PART 2 - COPY TO BE RETURNED WITH RESPONSE



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/680,963
Source: IFWO
Date Processed by STIC: 12/21/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED
SUGGESTED CORRECTION
SERIAL NUMBER: 10/680,963

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 Skipped Sequences
(NEW RULES) Sequence(s) 7-8 missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 *<This is the valid format for intentionally skipped sequences.*

9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

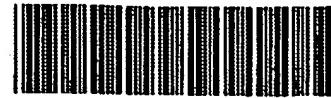
10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 Use of <220>

→ Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/680,963

DATE: 12/21/2004

TIME: 11:33:40

Input Set : A:\GFI-108 Sequence listing.ST25.txt
 Output Set: N:\CRF4\12212004\J680963.raw

3 <110> APPLICANT: GlycoFi, Inc.
 4 Bobrowicz, Piotr
 5 Hamilton, Stephen R.
 6 Gerngross, Tilman U.
 7 Wildt, Stefan
 8 Choi, Byung-Kwon
 9 Nett, Juergen H.
 10 Davidson, Robert C.
 12 <120> TITLE OF INVENTION: N-Acetylglucosaminyltransferase III expression in lower eukaryotes
 13
 15 <130> FILE REFERENCE: GFI-108 CIP
 17 <140> CURRENT APPLICATION NUMBER: US 10/680,963
 18 <141> CURRENT FILING DATE: 2003-10-07
 20 <150> PRIOR APPLICATION NUMBER: US 10/371,877
 21 <151> PRIOR FILING DATE: 2003-02-20
 23 <150> PRIOR APPLICATION NUMBER: US 09/892,591
 24 <151> PRIOR FILING DATE: 2001-06-27
 26 <150> PRIOR APPLICATION NUMBER: US 60/214,358
 27 <151> PRIOR FILING DATE: 2000-06-28
 29 <150> PRIOR APPLICATION NUMBER: US 60/215,638
 30 <151> PRIOR FILING DATE: 2000-06-30
 32 <150> PRIOR APPLICATION NUMBER: US 60/279,997
 33 <151> PRIOR FILING DATE: 2001-03-30
 35 <150> PRIOR APPLICATION NUMBER: PCT/US02/41510
 36 <151> PRIOR FILING DATE: 2002-12-24
 38 <150> PRIOR APPLICATION NUMBER: US 60/344,169
 39 <151> PRIOR FILING DATE: 2001-12-27
 41 <160> NUMBER OF SEQ ID NOS: 101
 43 <170> SOFTWARE: PatentIn version 3.2
 45 <210> SEQ ID NO: 1
 46 <211> LENGTH: 3
 47 <212> TYPE: PRT
 48 <213> ORGANISM: artificial
 50 <220> FEATURE:
 51 <223> OTHER INFORMATION: Glycosylation target
 54 <220> FEATURE:
 55 <221> NAME/KEY: MISC_FEATURE
 56 <222> LOCATION: (2)...(2)
 57 <223> OTHER INFORMATION: wherein "Xaa" is any amino acid except proline
 59 <400> SEQUENCE: 1
 61 Asn Xaa Ser
 62 1
 65 <210> SEQ ID NO: 2

PR 1-3,6
Does Not Comply
Corrected Diskette Needed

give source of genetic material
(see item 11 on Error Summary
Sheet)

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/680,963

DATE: 12/21/2004
TIME: 11:33:40

Input Set : A:\GFI-108 Sequence listing.ST25.txt
Output Set: N:\CRF4\12212004\J680963.raw

66 <211> LENGTH: 3
 67 <212> TYPE: PRT
 68 <213> ORGANISM: artificial
 70 <220> FEATURE:
 71 <223> OTHER INFORMATION: Glycosylation target same error
 74 <220> FEATURE:
 75 <221> NAME/KEY: MISC_FEATURE
 76 <222> LOCATION: (2)..(2)
 77 <223> OTHER INFORMATION: wherein "Xaa" is any amino acid except proline
 79 <400> SEQUENCE: 2
 W--> 81 Asn Xaa Thr
 82 1
 85 <210> SEQ ID NO: 3
 86 <211> LENGTH: 21
 87 <212> TYPE: DNA
 88 <213> ORGANISM: artificial
 90 <220> FEATURE:
 91 <223> OTHER INFORMATION: Primer A for target gene in P. pastoris (1,6-mannosyltransferase)
 93 <400> SEQUENCE: 3
 94 atggcgaagg cagatggcag t 21
 97 <210> SEQ ID NO: 4
 98 <211> LENGTH: 21
 99 <212> TYPE: DNA
 100 <213> ORGANISM: artificial
 102 <220> FEATURE:
 103 <223> OTHER INFORMATION: Primer B for target gene in P. pastoris (1,6-mannosyltransferase)
 105 <400> SEQUENCE: 4
 106 tttagtccttc caacttcctt c 21
 109 <210> SEQ ID NO: 5
 110 <211> LENGTH: 26
 111 <212> TYPE: DNA
 112 <213> ORGANISM: artificial
 114 <220> FEATURE:
 115 <223> OTHER INFORMATION: Primer A for target gene in P. pastoris (1,2-mannosyltransferases)
 119 <220> FEATURE:
 120 <221> NAME/KEY: misc_feature
 121 <222> LOCATION: (9)..(9)
 122 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
 124 <220> FEATURE:
 125 <221> NAME/KEY: misc_feature
 126 <222> LOCATION: (12)..(12)
 127 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
 129 <220> FEATURE:
 130 <221> NAME/KEY: misc_feature
 131 <222> LOCATION: (18)..(18)
 132 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
 134 <400> SEQUENCE: 5
 W--> 135 taytggmgng tngarcynga yathaa 26

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/680,963

DATE: 12/21/2004
TIME: 11:33:40

Input Set : A:\GFI-108 Sequence listing.ST25.txt
Output Set: N:\CRF4\12212004\J680963.raw

138 <210> SEQ ID NO: 6
 139 <211> LENGTH: 20
 140 <212> TYPE: DNA
 141 <213> ORGANISM: artificial
 143 <220> FEATURE:
 144 <223> OTHER INFORMATION: Primer B for target gene in P. pastoris (1,2
 145 mannosyltransferases)
 148 <220> FEATURE:
 149 <221> NAME/KEY: misc_feature
 150 <222> LOCATION: (6)..(6)
 151 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
 153 <220> FEATURE:
 154 <221> NAME/KEY: misc_feature
 155 <222> LOCATION: (12)..(12)
 156 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
 158 <400> SEQUENCE: 6
 W--> 159 gertcncccc anckytcrtta 20
 162 <210> SEQ ID NO: 7
 163 <211> LENGTH: 0
 164 <212> TYPE: DNA
 165 <213> ORGANISM: Kluyveromyces lactis
 167 <400> SEQUENCE: 7
 W--> 168 000
 170 <210> SEQ ID NO: 8
 171 <211> LENGTH: 0
 172 <212> TYPE: PRT
 173 <213> ORGANISM: Kluyveromyces lactis
 175 <400> SEQUENCE: 8
 W--> 176 000
 178 <210> SEQ ID NO: 9
 179 <211> LENGTH: 458
 180 <212> TYPE: PRT
 181 <213> ORGANISM: Saccharomyces cerevisiae
 184 <220> FEATURE:
 185 <221> NAME/KEY: MISC_FEATURE
 186 <222> LOCATION: (304)..(318)
 187 <223> OTHER INFORMATION: Low-complexity sequence
 189 <220> FEATURE:
 190 <221> NAME/KEY: MISC_FEATURE
 191 <222> LOCATION: (416)..(436)
 192 <223> OTHER INFORMATION: Low-complexity sequence same error
 194 <400> SEQUENCE: 9
 196 Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
 197 1 5 10 15
 200 Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
 201 20 25 30
 204 Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
 205 35 40 45
 208 Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Lys Lys

*delete this section
(see item 8 on Error Summary Sheet)
for valid format*

*Do the same with
sequences 43 and 44*

*yes, but which amino acid(s) do
the Xaa's represent?*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/680,963

DATE: 12/21/2004

TIME: 11:33:40

Input Set : A:\GFI-108 Sequence listing.ST25.txt

Output Set: N:\CRF4\12212004\J680963.raw

209	50	55	60
212	Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu		
213	65	70	75
216	Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly		80
217	85	90	95
220	Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met		
221	100	105	110
224	Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val		
225	115	120	125
228	Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys		
229	130	135	140
232	Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu		
233	145	150	155
236	Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys		160
237	165	170	175
240	Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala		
241	180	185	190
244	Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val		
245	195	200	205
248	Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu		
249	210	215	220
252	Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala		
253	225	230	235
256	Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln		240
257	245	250	255
260	Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu		
261	260	265	270
264	His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile		
265	275	280	285
W-->	268 Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe Xaa		
269	290	295	300
272	Xaa Phe Val		
273	305	310	315
276	Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His		320
277	325	330	335
280	Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile		
281	340	345	350
284	Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg		
285	355	360	365
288	Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile		
289	370	375	380
292	Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr		
293	385	390	395
296	Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Xaa		400
297	405	410	415
300	Xaa		
301	420	425	430
304	Xaa Xaa Xaa Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg		
305	435	440	445

RAW SEQUENCE LISTING DATE: 12/21/2004
 PATENT APPLICATION: US/10/680,963 TIME: 11:33:40

Input Set : A:\GFI-108 Sequence listing.ST25.txt
 Output Set: N:\CRF4\12212004\J680963.raw

308 Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
 309 450 455
 312 <210> SEQ ID NO: 10
 313 <211> LENGTH: 458
 314 <212> TYPE: PRT
 315 <213> ORGANISM: *Saccharomyces cerevisiae*
 317 <400> SEQUENCE: 10
 319 Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
 320 1 5 10 15
 323 Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
 324 20 25 30
 327 Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
 328 35 40 45
 331 Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
 332 50 55 60
 335 Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
 336 65 70 75 80
 339 Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
 340 85 90 95
 343 Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
 344 100 105 110
 347 Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
 348 115 120 125
 351 Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
 352 130 135 140
 355 Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
 356 145 150 155 160
 359 Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
 360 165 170 175
 363 Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
 364 180 185 190
 367 Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
 368 195 200 205
 371 Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
 372 210 215 220
 375 Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
 376 225 230 235 240
 379 Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
 380 245 250 255
 383 Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
 384 260 265 270
 387 His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
 388 275 280 285
 391 Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His
 392 290 295 300
 395 Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val
 396 305 310 315 320
 399 Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
 400 325 330 335

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/680,963

DATE: 12/21/2004
TIME: 11:33:41

Input Set : A:\GFI-108 Sequence listing.ST25.txt
Output Set: N:\CRF4\12212004\J680963.raw

::61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
::81 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
::135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
::159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
::168 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:
::176 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE:
::268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:288
I:341 Repeated in SeqNo=9
::516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:272
I:341 Repeated in SeqNo=11
::1467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:208
I:341 Repeated in SeqNo=25
::1692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:176
I:341 Repeated in SeqNo=27
::1909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:160
I:341 Repeated in SeqNo=29
::2126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:160
I:341 Repeated in SeqNo=31
::2547 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (43) SEQUENCE:
::2555 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (44) SEQUENCE:
::3343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75 after pos.:0

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/680,963

DATE: 12/21/2004

TIME: 11:33:41

Input Set : A:\GFI-108 Sequence listing.ST25.txt
Output Set: N:\CRF4\12212004\J680963.raw

::61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
::81 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
::135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
::159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
::168 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:
::176 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE:
::268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:288
I:341 Repeated in SeqNo=9
::516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:272
I:341 Repeated in SeqNo=11
::1467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:208
I:341 Repeated in SeqNo=25
::1692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:176
I:341 Repeated in SeqNo=27
::1909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:160
I:341 Repeated in SeqNo=29
::2126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:160
I:341 Repeated in SeqNo=31
::2547 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (43) SEQUENCE:
::2555 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (44) SEQUENCE:
::3343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75 after pos.:0

Organization _____ Bldg./Room _____

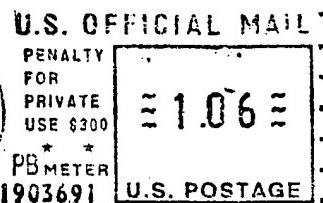
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